B1 Cont Nucleic Acids Research 22: 4673, 1994) and the alignment of the RNase P sequences of the present invention (SEQ ID NOs: 39-95).

Please replace the paragraph on page 10, line 27 through page 11, line 8 of the specification with the following paragraph that has been re-written in clean form.

B2 This RNase P consensus sequence was derived as follows. We aligned the sequences of the known bacterial RNase P protein subunits using the ClustalW alignment program (Thompson et al., *supra*) (see Fig. 1, the previously known RNase P sequences were obtained from the RNase P database; www.jwbrown.mbio.ncsu.edu/rnasp/home.html.) This ClustalW alignment was then manually refined to align highly conserved RNase P hydrophobic and basic residues that had been demonstrated by mutation studies to be important for RNase P catalytic function (Gopalan et al., J. Mol. Biol. 267: 818, 1997). The spacing between the conserved residues, as well as the identity of the individual residues, appears critical to RNase P function.

Please replace the paragraph on page 11, lines 9-25, of the specification with the following paragraph that has been re-written in clean form.

B3 Twenty amino acids were identified as highly conserved (shown as the shaded residues in Fig. 1). The percent of RNase P sequences which conserve each of the shaded residues is shown below the sequence information as percent identity. Based upon these known sequences, we determined that a polypeptide identified by our above-described RNase P BLAST search contained an RNase consensus sequence and was a genuine RNase P protein subunit if it contained at least nine of the above-described twenty amino acids. Preferred polypeptides have a consensus sequence with at least 13 of the amino acids and/or conserve at least seven of the following subset of amino acids: F18, R46, K53, A59, R62, N63, K66, R67, and R70. This subset of amino acids is preferred because it has been identified as playing a significant role in RNase P function through mutation studies (Gopalan et al., J. Mol. Biol. 267: 818 1997) and the determination of the RNase P three dimensional structure (Stams et al., Science 280: 752, 1998). [As shown in Fig. 2, the] The three dimensional structure reveals that all of the residues that make up the above-described nine amino acid subset are proximal to each other in the tertiary structure of the protein, despite the distance between some of the residues in the primary structure.

Please replace the paragraph on page 12, lines 9-14, of the specification with the following paragraph that has been re-written in clean form.

B4

All of the novel RNase P protein sequences were identified by the above-described BLAST search. The alignment of these sequences with the known RNase P sequences is also shown in Fig. 1. This alignment demonstrates that the amino acid sequences of the invention all contain RNase P consensus sequences. Therefore, these polypeptides are genuine RNase P proteins.

Please replace the paragraph on page 22, lines 10-21, of the specification with the following paragraph that has been re-written in clean form.

B5

The preferred reaction buffer contains 50 mM Tris-HCl (pH 7.5), 100 mM ammonium chloride and 10 mM magnesium chloride. Concentrations of 10-100 mM, 25-500 mM and 1-100 mM of the above, respectively, can be substituted, as can other buffering agents such as MOPS or HEPES, or other monovalent cations, such as sodium or potassium. When the assay is run in either 98 or 384-well polystyrene or polypropylene assay plates, there is a very significant decrease in the fluorescence intensity and polarization of the annealed substrate over time in the absence of enzyme. Various conditions have been tested to prevent the loss of signal with time. The preferred conditions include addition of 10-40 μg/ml carbonic anhydrase and 10-100 μg/ml polyC to the buffer. Other materials, such as, 0.5-5% glycerol, 10-100 μg/ml hen egg lysozyme, 10-50 μg/mL tRNA, 1-10 mM DTT, or 2-10 mM DTT can also be added to the buffer to prevent some loss of signal.

In the claims:

Cancel claims 3-7 and 12, without prejudice, and replace claims 1, 9, and 13 with the following amended claims that have been re-written in clean form.

B6

1. (Amended) An isolated polypeptide comprising an RNase P consensus sequence wherein said polypeptide has RNase P protein activity, wherein said polypeptide is a bacterial polypeptide, and wherein said polypeptide is not a polypeptide from one of the following organisms: Coxiella burnetii (None Mile) U10529, Rickettsia prowazekii (Madrid E) AJ235272, Neisseria meningitidis (Z2491) AL162753, Neisseria meningitidis